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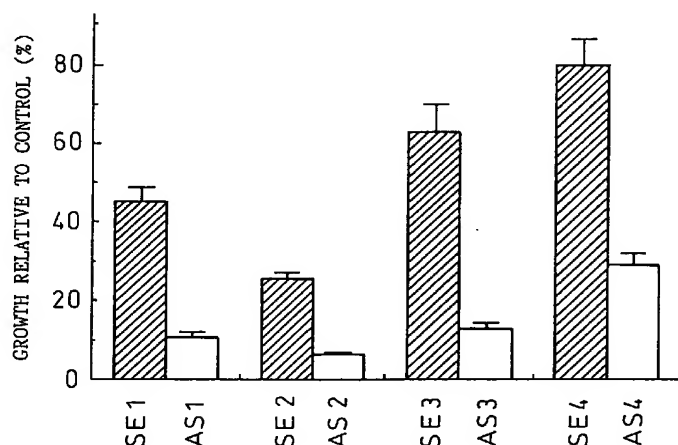
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(54) LEUKEMIC CELL GROWTH INHIBITOR CONTAINING ANTISENSE OLIGONUCLEOTIDE DERIVATIVE AGAINST WILMS' TUMOR GENE (WT1)

(57) A leukemic cell growth inhibitor containing anti-sense oligonucleotide derivatives against Wilms' tumor

gene (WT1).

Fig.1



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Description

Technical Field

5 The present invention relates to a growth inhibitor for leukemia cells comprising an antisense nucleotide derivative.

Background Art

10 Wilms' tumor is a pediatric kidney tumor that occurs as a result of deactivation of both allele of the Wilms' tumor gene (WT1) located on chromosome 11p13 (Call, K.M., et al., Cell 60: 509, 1990). A non-coding upstream sequence of WT1 (C.E. Campbell, et al., Oncogene 9: 583-595, 1994) and a coding region that includes the intron (D.A. Haber, et al., Proc. Natl. Acad. Sci. USA, 88: 9618-9622, 1991) have previously been reported, and they are expected to be involved in the growth and differentiation of the tumor and so forth (D.A. Haber, et al., Proc. Natl. Acad. Sci. USA, 88: 9618-9622, 1991).

15 However, it was not known that WT1 is involved in the growth of leukemia cells, and that an antisense oligonucleotide derivative to WT1 suppresses and inhibits growth of leukemia cells.

Disclosure of the Invention

20 Thus, the present invention provides a growth inhibitor for leukemia cells comprising an antisense nucleotide derivative to Wilms' tumor gene (WT1).

Brief Description of the Drawings

25 Fig. 1 is a graph showing the inhibitory effects of oligonucleotide on the growth of leukemia cell line K562.

Fig. 2 is a graph showing the relationship between the concentrations of oligonucleotides SE3 and AS3 and the growth of leukemia cell line K562.

Fig. 3 is a graph showing the relationship between the concentrations of oligonucleotides SE4 and AS4 and the growth of leukemia cell line K562.

30 Fig. 4 is a graph showing the time-based effects of oligonucleotides SE3 and AS3 on the growth of leukemia cell line K562.

Fig. 5 is a graph showing the effects of various oligonucleotides on the growth of leukemia cell line K562.

Fig. 6 is a graph showing the inhibitory effects of various oligonucleotides on the growth of leukemia cell line HEL positive for expression of WT1.

35 Fig. 7 is a graph showing the inhibitory effects of various oligonucleotides on the growth of leukemia cell line THP-1 positive for expression of WT1.

Fig. 8 is a graph showing the inhibitory effects of various nucleotides on the growth of malignant lymphoma cell line U937 negative for expression of WT1.

40 Fig. 9 is a graph showing the effects of oligonucleotides SE3 and AS3 on the formation of leukemia cell colonies from bone marrow mononuclear cells derived from leukemia patients.

Fig. 10 is a graph showing the effects of oligonucleotides SE3 and AS3 on the formation of granulocytic macrophage colonies from bone marrow mononuclear cells derived from healthy volunteers.

45 Fig. 11, panel A is a photograph of the results of electrophoresis indicating a decrease in the level of WT1 protein in cells in the case of adding various WT1 antisense oligonucleotides to a culture of K562 cells; panel B indicates a decrease in the level of WT1 protein in cells in the case of adding WT1 antisense oligonucleotides to fresh leukemia cells from a patient with AML.

Detailed Description of the Invention

50 The present invention provides a leukemia cell growth inhibitor comprising an antisense oligonucleotide derivative to WT1. The antisense oligonucleotide derivatives used in the present invention is an antisense oligonucleotide derivative to WT1, examples of which include that to the transcription capping site of WT1, gene that to the translation starting region, that to an exon or that to an intron.

55 For example, a nucleotide sequence of a sense DNA strand of the region containing the transcription capping site of WT1 is represented with SEQ ID NO: 9. In addition, a nucleotide sequence of a sense DNA strand of exons 1 to 10 of the region coding for WT1 is represented with SEQ ID NO: 10 to 19. The present invention uses an antisense oligonucleotide derivative to such a nucleotide sequence of the sense DNA strand of WT1. This antisense oligonucleotide derivative is an antisense oligonucleotide derivative comprising 5 to 50 continuous nucleotides and preferably 9 to 30

nucleotides of antisense DNA or RNA chain for WT1, or 5 to 70 nucleotides and preferably 9 to 50 nucleotides intermittently or partially complementary to DNA or RNA chain for WT1 and capable of binding to DNA or RNA chain for WT1.

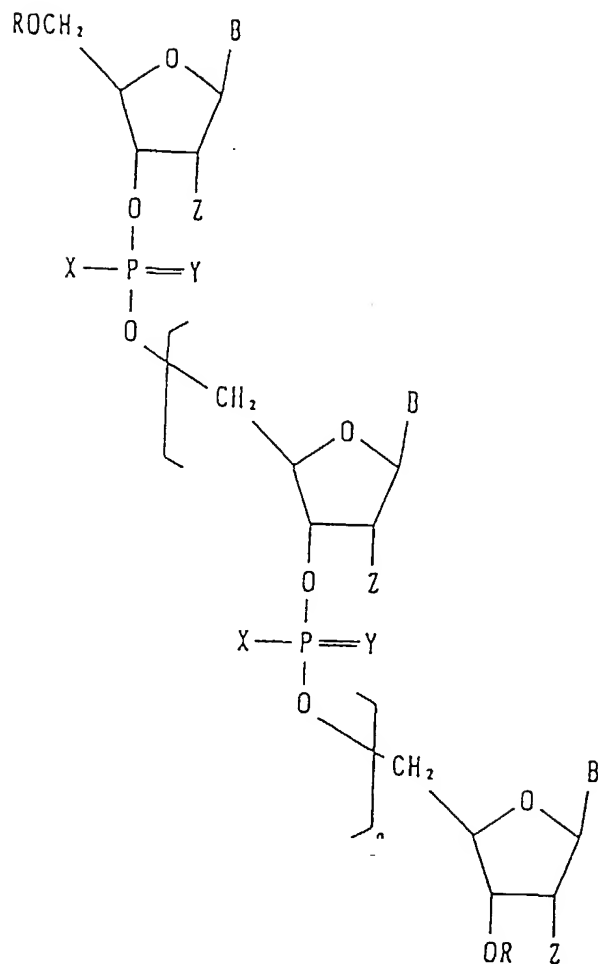
Examples of antisense oligonucleotide derivatives to the transcription capping site include those having the following nucleotide sequences: 5'-AGGGTCGAATGCGGTGGG-3' (SEQ ID NO: 2) and 5'-TCAAATAAGAGGGGCCGG-3' (SEQ ID NO: 4). In addition, examples of antisense oligonucleotide derivatives to the translation starting region include antisense oligonucleotide derivatives to the translation starting codon ATG and its upstream and/or downstream region such as the following nucleotide sequence: 5'-GTCGGAGCCCATTTGCTG-3' (SEQ ID NO: 6).

In addition, ten exons are contained in the region coding for WT1, and examples of the antisense oligonucleotide derivative of the present invention include those to the sequences contained in any of these exons, those to the sequences extending over any two consecutive exons after splicing or those to the sequences extending over a consecutive intron and exon, and those to sequences of all introns and the 3' and 5' non-coding regions. One example of an antisense oligonucleotide derivative is that to the 6th exon, an example of which is that to the following nucleotide sequence: 5'-CGTTGTGTGGTTATCGCT-3' (SEQ ID NO: 8).

Moreover, although there are no particular restrictions on the region corresponding to the antisense oligonucleotide derivative of the present invention having a nucleotide sequence intermittently or partially complementary to the DNA or RNA chain for WT1, those similar to ribozymes having a function to cleave the DNA chain or RNA chain for WT1 are included in these.

The structure of antisense oligonucleotide derivative used in the present invention is as shown in chemical formula 1, wherein X may independently be an oxygen (O), sulfur (S), lower alkyl group, primary amine or secondary amine. Y may independently be an oxygen (O) or sulfur (S). Z is a hydrogen atom or hydroxyl group. B is chosen from adenine, guanine, thymine or cytosine when Z is a hydrogen atom, or chosen from adenine, guanine, uracil or cytosine when Z is a hydroxyl group, and is mainly an oligonucleotide complementary to DNA or mRNA coding for WT1. R is independently a hydrogen atom, dimethoxytrityl group or lower alkyl group. N is an integer of 7-28.

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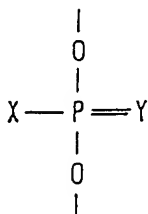
Chemical Formula 1

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45

Preferable examples of antisense oligonucleotide derivatives include not only non-modified antisense oligonucleotides, but also modified antisense oligonucleotides. Examples of these modified forms include low alkyl phosphonate forms like the above-mentioned methylphosphonate form or ethylphosphonate form, and other phosphorothioate forms or phosphoroamidate forms (see chemical formula 2).

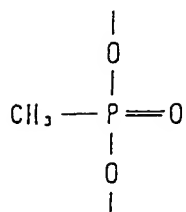
Example of

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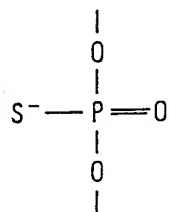
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Methyl phosphonate



10

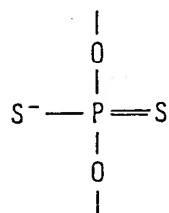
Phosphorothioate



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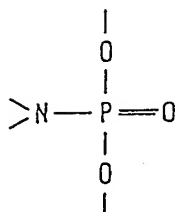
Phosphorodithioate



25

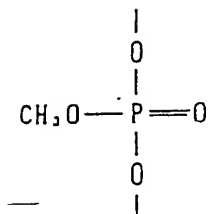
30

Phosphoroamidate



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Triester phosphate



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Chemical Formula 2

These antisense oligonucleotide derivatives can be obtained according to the following conventional methods.

50 The antisense oligonucleotides in which X and Y in chemical formula 1 are O and Z is a hydrogen atom or hydroxyl group are easily synthesized by a commercially available DNA synthesizer (for example, that manufactured by Applied Biosystems).

Antisense oligodeoxyribonucleotide in which Z is a hydrogen atom can be obtained by a method such as solid phase synthesis using phosphoroamidite or solid phase synthesis using hydrogen phosphonate.

55 See, for example, T. Atkinson and M. Smith in Oligonucleotide Synthesis: A Practical Approach, ed. M.J. Gait, IRL Press, 35-81 (1984); M.H. Caruthers, Science, 230, 281 (1985); A. Kume, M. Fujii, M. Sekine and M. Hata, J. Org. Chem., 49, 2139 (1984); B.C. Froehler and M. Matteucci, Tetrahedron Lett., 27, 469 (1986); P.J. Garegg, I. Lindh, T. Regberg, J. Stawinski, R. Stromberg and C. Henrichson, ibid., 27, 4051 (1986); B.S. Sproat and M.J. Gait in Oligonucleotide Synthesis: A Practical Approach, ed. M.J. Gait, IRL Press, 83-115 (1984); S.L. Beaucage and M.H. Caruthers,

Tetrahedron Lett., 22, 1859-1862 (1981); M.D. Matteucci and M.H. Caruthers, Tetrahedron Lett., 21, 719-722 (1980); and, M.D. Matteucci and M.H. Caruthers, J. Am. Chem. Soc., 103, 3185-3191 (1981).

Triester phosphate modified forms, in which X is a lower alkoxy group, can be obtained by ordinary methods, such as treatment of an oligonucleotide obtained by chemical synthesis with a tosylchloride solution of DMF, methanol and 2,6-lutidine (Moody H.M., et al., Nucleic Acids Res., 17, 4769-4782 (1989)).

Alkylphosphonate modified forms, in which X is an alkyl group, can be obtained by ordinary methods using, for example, phosphoramidite (M.A. Dorman, et al., Tetrahedron, 40, 95-102 (1984); and, K.L. Agarwal and F. Rittina, Nucleic Acids Res., 6, 3009-3024 (1979)).

Phosphorothioate modified forms in which X is S can be obtained by ordinary methods such as solid phase synthesis using sulfur (C.A. Stein, et al., Nucleic Acids Res., 16, 3209-3221 (1988) or solid phase synthesis using tetraethylthiolam disulfide (H. Vu and B.L. Hirschbein, Tetrahedron Letters, 32, 3005-3008 (1991)).

Phosphorodithioate modified forms in which X and Y are both S can be obtained by, for example, solid phase synthesis by converting bis-amidite to thioamidite and allowing sulfur to act on the thioamidite (W.K.D. Brill, et al., J. Am. Chem. Soc., 111, 2321-2322 (1989)).

Phosphoramidate modified forms in which X is a primary amine or secondary amine can be obtained by, for example, solid phase synthesis by treating hydrogen phosphonate with a primary or secondary amine (B. Froehler, et al., Nucleic Acids Res., 16, 4831-4839 (1988)), or by oxidizing amidite with tert-butyl hydroperoxide (H. Ozaki, et al., Tetrahedron Lett., 30, 5899-5902 (1989)).

Although synthesis of antisense oligoribonucleotide in which Z is a hydroxyl group is extremely difficult in comparison with synthesis of antisense oligodeoxyribonucleotide since the 2'-hydroxyl group on ribose (sugar) must be protected, it can be synthesized by suitably selecting the protecting group and phosphorylation method (see, Basic Microbiology Course, Vol. 8, Genetic Engineering, E. Ohtsuka, K. Miura, ed. T. Ando and K. Sakaguchi, Oct. 10, 1987, Kyoritsu Publishing Co., Ltd.).

Purification and confirmation of purity can be performed by high-performance liquid chromatography and polyacrylamide gel electrophoresis. Confirmation of molecular weight can be performed by Electrospray Ionization Mass Spectrometry or Fast Atom Bombardment-Mass Spectrometry.

The antisense oligonucleotide derivatives of the present invention acts at any stage from genomic DNA to mature mRNA, and suppression of its expression is thought to inhibit growth of leukemia cells. Thus, the antisense oligonucleotides of the invention of the present application is expected to be effective in the treatment of leukemia.

Moreover, as will be described later, the antisense oligonucleotide derivatives of the present invention is thought to specifically inhibit leukemia cells without inhibiting the growth of normal bone marrow cells. Thus, it can also be applied to "autologous bone marrow transplantation" and "autologous peripheral blood stem cell transplantation" in which, for example, after first removing bone marrow cells or peripheral blood stem cells from the body and treating them in vitro with the antisense oligonucleotide derivatives of the present invention to inhibit the growth of leukemia cells, only normal bone marrow cells or normal peripheral blood stem cells are returned to the body.

The antisense oligonucleotide derivatives of the present invention can also be used in the form of an external preparation such as a liniment or poultice by mixing with a suitable inactive base.

In addition, the antisense oligonucleotide derivatives of the present invention can also be used in the form of tablets, powders, granules, capsules, liposome capsules, injection preparations, liquids or nose drops by adding a vehicle, isotonic agent, solubility assistant, stabilizer, preservative or analgesic and so forth as necessary, or can be made into a freeze-dried preparation. These formulations can be prepared in accordance with routine methods.

The antisense oligonucleotide derivatives of the present invention can be applied directly to the affected area of the patients, or applied so as to be able to reach the affected area as a result of intravascular administration and so forth. Moreover, antisense inclusion materials can also be used to improve duration and membrane permeation. Examples of these include liposomes, poly-L-lysine, lipids, cholesterol lipofectin and their derivatives.

The dose of the antisense oligonucleotide derivative of the present invention is such that a preferable amount can be used by suitably preparing a dose according to the patient's condition, age, sex and body weight. In addition, the administration method can be suitably selected from various administration methods, including oral administration, intramuscular administration, intraperitoneal administration, intradermal administration, subcutaneous administration, intravenous administration, intraarterial administration and rectal administration according to the patient's conditions, the drug forms and so forth.

The following provides a detailed explanation of the present invention through Examples.

Examples

Synthesis Example 1

The oligodeoxyribonucleotides used below (SEQ ID NOS: 1 to 8) were synthesized using an automatic synthesizer

(Applied Biosystems), purified by high-performance liquid chromatography, precipitated three times with ethanol, and suspended in phosphate buffer. The synthesized oligonucleotides were as listed below.

- SEQ ID NO: 1: Sense sequence of transcription capping site (SE1)
- SEQ ID NO: 2: Antisense sequence of transcription capping site (AS1)
- SEQ ID NO: 3: Sense sequence of transcription capping region (SE2)
- SEQ ID NO: 4: Antisense sequence of transcription capping region (AS2)
- SEQ ID NO: 5: Sense sequence of translation starting region (SE3)
- SEQ ID NO: 6: Antisense sequence of translation starting region (AS3)
- SEQ ID NO: 7: Sense sequence of exon 6 (SE4)
- SEQ ID NO: 8: Antisense sequence of exon 6 (AS4)

Example 1

5 x 10⁴ cells/ml of leukemia cell line K562 positive for WT1 expression were inoculated into RPMI 1640 medium not containing fetal calf serum (FCS) contained in the wells of a flat-bottom 96-well plate in the amount of 100 µl/well. Each oligonucleotide was added to a series of three wells to a final concentration of 200 µg/well. After incubating for 2 hours, FCS was added to each well to a final concentration of 10%. Oligonucleotides were then added to the culture in an amount equal to half the above-mentioned amount every 24 hours.

After culturing for 96 hours, the numbers of viable cells were counted using the pigment elimination method. An equal volume of PBS not containing nucleotide was added as the control culture, and the number of cells of this control culture was taken to be 100%.

The results are shown in Fig. 1. As is clear from this figure, all of the antisense oligonucleotides powerfully inhibited cell growth in comparison with the corresponding sense oligonucleotides.

Example 2

The same experiment as that described in Example 1 was performed, but oligonucleotides SE3 and AS3 were added at various concentrations. As is clear from Fig. 2, although sense oligonucleotide (SE3) virtually did not inhibit cell growth, antisense oligonucleotide (AS3) inhibited cell growth in a dose dependent manner.

Example 3

The same experiment as that described in Example 1 was performed, but oligonucleotides SE4 and AS4 were added at various concentrations. As is clear from Fig. 3, although sense oligonucleotide (SE4) virtually did not inhibit cell growth, antisense oligonucleotide (AS4) inhibited cell growth in a dose dependent manner.

Example 4

The same experiment as described in Example 1 was performed. However, the cells were cultured in a flat-bottom 24-well plate at a concentration of 5 x 10⁴ cells/ml and in the amount of 1 ml/well. Oligonucleotides SE3 and AS3 were added and the numbers of viable cells were counted daily for 2 to 5 days. The results are shown in Fig. 4. As is clear from the figure, although cell growth similar to the control was observed in the case of adding sense oligonucleotide, in the case of adding antisense oligonucleotide, cell growth was inhibited.

Example 5

The same experiment as described in Example 1 was performed. However, SE3, AS3, an antisense oligonucleotide 5'-AGAGAAGAAGGGAACCCC-3' (SEQ ID NO: 20) (MPO-AS) to myeloperoxidase (MPO) gene, and an antisense oligonucleotide 5'-GCGTGGGCAGCCTGGGAA-3' (SEQ ID NO: 21) (FV-AS) to blood coagulation factor V (FV) were used for the oligonucleotides. As is clear from Fig. 5, cell growth was inhibited only in the case of using AS3.

Example 6

The same experiment as described in Example 1 was performed, but WT1 expression-positive cell lines HEL and THP-1 as well as WT1 expression-negative cell line U937 were used as the experimental cells. The same eight types of oligonucleotides used in Example 1 were used as the oligonucleotides. In the case of using WT1 expression-positive cell line HEL (Fig. 6) or THP-1 (Fig. 7), cell growth was inhibited by antisense oligonucleotide. In contrast, in the case

of using WT1 expression-negative cell line U937 (Fig. 8), cell growth was not inhibited even if antisense oligonucleotide was added.

Example 7

Bone marrow cells from leukemia patients and healthy volunteers were treated with heparin and suspended in RPMI 1640 medium to obtain bone marrow mononuclear cells by Ficoll-Hypaque density gradient centrifugation. A protein (100 μ l/well) of the above-mentioned mononuclear cells at a cell density of 1.5×10^6 cells/ml were added to a flat-bottom 96-well plate containing α -MEM containing GM-CSF (100 ng/ml) and IL-3 (100 units/ml). Treatment with oligonucleotides (SE3 and AS3) was performed in the same manner as Example 1.

After 96 hours, the cells were collected and plated in methylcellulose medium [1.2% methylcellulose α -MEM, 20% FCS, GM-CSF (100 ng/ml), G-CSF (100 ng/ml), IL-3 (100 units/ml) and SCF (10 ng/ml)]. Culturing was performed in three series. The number of leukemia cell colonies (CFU-L) and granulocytic macrophage colonies (CFU-GM) were counted on day 14.

Fig. 9 shows the morphology of the leukemia colonies in samples from four leukemia patients (two acute myeloid leukemia (AML) patients and 2 chronic myeloid leukemia (CML) patients). The formation of colonies can be seen to be inhibited by antisense oligonucleotide. Fig. 10 shows the appearance of granulocytic macrophage colonies in samples from healthy volunteers. Colony formation is not inhibited by either of the antisense oligonucleotides.

Example 8

Random oligonucleotide, oligonucleotide AS1, oligonucleotide AS2 or oligonucleotide AS3 was added at a concentration of 200 μ g/ml to K562 cells (A) or fresh leukemia cells from a patient with AML (B) at a cell density of 5×10^4 cells/well in a 24-well plate, followed by addition of the oligonucleotides at a concentration of 100 μ g/ml every 24 hours. The cells were harvested 4 days after the initial treatment with oligonucleotide, washed with PBS and lysed with Laemli sample buffer.

Each cell lysate from 2×10^4 cells was boiled for 5 minutes, and then applied to each lane of 5% dodecylsodium sulfate-polyacrylamide gel. Following electrophoresis, the proteins were transferred to an Immobilon polyvinylidene difluoride filter (Millipore Corp. MA, USA). This filter was then probed using an anti-WT1 polyclonal antibody to synthetic polypeptide (amino acid positions 177 to 192: Lys His Glu Asp Pro Met Gly Gln Gln Gly Ser Leu Gly Glu Gln Gln (SEQ ID NO: 22)). This was followed by treatment with horseradish peroxidase-bound anti-immunoglobulin antibody (Amersham, Little Chalfont, U.K.). After washing, the filter was immersed in detection reagent (Amersham, Little Chalfont, U.K.) for 1 hour followed by autoradiography treatment for 1 to 5 minutes.

After washing twice with TBST (Tris buffer containing 0.05% Tween 20), the filter was probed with anti-actin monoclonal antibody (Oncogene Science Inc., NY, USA) followed by autoradiography in the manner described above.

The density of the bands corresponding to WT1 protein and actin were measured with a CS-9000 densitometer (Shimizu, Kyoto) followed by calculation of the WT1/actin ratio.

The results are shown in Fig. 11 A and B. In these figures, lane 1 shows the results in the case of adding random oligonucleotide, lane 2 the case of adding oligonucleotide AS3, lane 3 the case of adding oligonucleotide AS1, and lane 4 the case of adding oligonucleotide AS2. In these figures, A indicates the results in the case of using K562 cells, while B indicates those in the case of using fresh leukemia cells from a patient with AML.

As is clear from Fig. 11A, in the case of adding WT1 oligonucleotide to medium containing K562 cells, the level of WT1 protein decreased significantly. On the other hand, control in the form of random nucleotide did not affect the level of WT1 protein. In addition, as is clear from Fig. 11B, in the case of adding WT1 oligonucleotide to medium containing leukemia cells recently isolated from a patient with AML, the level of WT1 protein decreased significantly. These results clearly showed that WT1 antisense oligonucleotide specifically inhibits the growth of leukemia cells by decreasing the level of WT1 protein.

Industrial Applicability

As has been stated above, the antisense oligonucleotides of the present invention is effective in inhibiting the growth of leukemia cells, and is therefore expected to be useful as a novel leukemia treatment.

SEQUENCE LISTING

SEQ ID NO: 1

5

Sequence length: 18

Sequence type: Nucleic acid

Strandedness: Single strand

10

Molecular type: Synthetic DNA

Sequence:

CCCACCGCAT TCGACCCT

SEQ ID NO: 2

15

Sequence length: 18

Sequence type: Nucleic acid

Strandedness: Single strand

20

Molecular type: Synthetic DNA

Sequence:

AGGGTCGAAT GCGGTGGG

SEQ ID NO: 3

25

Sequence length: 18

Sequence type: Nucleic acid

Strandedness: Single strand

30

Molecular type: Synthetic DNA

Sequence:

CCGGCCCCTC TTATTGA

SEQ ID NO: 4

35

Sequence length: 18

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

40

Sequence:

TCAAATAAGA GGGGCCCG

SEQ ID NO: 5

45

Sequence length: 18

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

50

Sequence:

CAGCAAATGG GCTCCGAC

SEQ ID NO: 6

55

Sequence length: 18

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence:

GTCGGAGCCC ATTTGCTG

SEQ ID NO: 7

Sequence length: 18

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence:

AGCGATAACC ACACAACG

SEQ ID NO: 8

Sequence length: 18

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence:

CGTTGTGTGG TTATCGCT

SEQ ID NO: 9

Sequence length: 1272

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence:

TGGTATCCTC	GACCAGGGCC	ACAGGCAGTG	CTCGGCGGAG	TGGCTCCAGG	AGTTACCCGC	60
TCCCTGCCGG	GCTTCGTATC	CAAACCTCC	CCTTCACCCC	TCCTCCCCAA	ACTGGGCGCC	120
AGGATGCTCC	GGCCGGAATA	TACGCAGGCT	TTGGGCGTTT	GCCAAGGGTT	TTCTTCCCTC	180
CTAAACTAGC	CGCTGTTTTC	CCGGCTTAAC	CGTAGAAGAA	TTAGATATTC	CTCACTGGAA	240
AGGGAAACTA	AGTGCTGCTG	ACTCCAATTT	TAGGTAGGCG	GCAACCGCCT	TCCGCCTGGC	300
GCAAACCTCA	CCAAGTAAAC	AACTACTAGC	CGATCGAAAT	ACGCCCGGCT	TATAACTGGT	360
GCAACTCCCG	GCCACCCAAC	TGAGGGACGT	TCGCTTTCAG	TCCCGACCTC	TGGAACCCAC	420
AAAGGGCCAC	CTCTTTCCCC	AGTGACCCCA	AGATCATGGC	CACTCCCCTA	CCCGACAGTT	480
CTAGAGCAAG	AGCCAGACTC	AAGGGTGCAA	AGCAAGGGTA	TACGCTTCTT	TGAAGCTTGA	540
CTGAGTTCTT	TCTGCGCTTT	CCTGAAGTTC	CCGCCCTCTT	GGAGCCTACC	TGCCCCTCCC	600
TCCAAACCAC	TCTTTTAGAT	TAACAACCCC	ATCTCTACTC	CCACCGCATT	CGACCCTGCC	660

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CGGACTCACT GCTACTGAAC GGACTCTCCA GTGAGACGAG GCTCCCACAC TGGCGAAGGC 720
AAGAAGGGGA GGTGGGGGA GGGTTGTGCC ACACCGGCCA GCTGAGAGCG CGTGTGGGT 780
5 TGAAGAGGAG GGTGTCTCCG AGAGGGACGC TCCCTCGGAC CCGCCCTCAC CCCAGCTGCG 840
AGGGCGCCCC CAAGGAGCAG CGCGCGCTGC CTGGCCGGGC TTGGGCTGCT GAGTGAATGG 900
AGCGGCCGAG CCTCCTGGCT CCTCCTCTTC CCCGCGCCGC CGGCCCTCT TATTTGAGCT 960
10 TTGGAAGCT GAGGGCAGCC AGGCAGCTGG GGTAAGGAGT TCAAGGCAGC GCCCACACCC 1020
GGGGCTCTC CGCAACCCGA CCGCCTGTGC CTCCCCACT TCCGCCCCTC CCTCCCACCT 1080
ACTATTAC CCACCCACCC ACCCAGAGCC GGGACGGCAG CCCAGGCGCC CGGGCCCCGC 1140
CGTCTCCTCG CCGGATCCT GGACTTCCTC TTGCTGCAGG ACCCGGCTTC CACGTGTGTC 1200
15 CCGGAGCCGG CGTCTCAGCA CACGCTCCGC TCCGGGCTG GGTGCCTACA GCAGCCAGAG 1260
CAGCAGGGAG TC 1272

SEQ ID NO: 10

Sequence length: 457

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence characteristic: Portion of exon 1 of WT1 gene

Sequence:

TCTGAGCCTC AGCAAATGGG CTCCGACGTG CGGGACCTGA ACGCGCTGCT GCCCGCCGTC 60
CCCTCCCTGG GTGGCGGCGG CGGCTGTGCC CTGCCTGTGA GCGGCGCGGC GCAGTGGGCG 120
30 CCGGTGCTGG ACTTTGCGCC CCGGGCGCT TCGGCTTACG GGTCTTGGG CGGCCCGCGC 180
CGGCCACCG CTCCGCGGCC ACCCCGCGC CCGCGCCTC ACTCCTTCAT CAAACAGGAG 240
CCGAGCTGGG GCGGCGCGGA GCCGCACGAG GAGCAGTGCC TGAGCGCCTT CACTGTCCAC 300
TTTTCCGGCC AGTTCAGTGG CACAGCCGGA GCCTGTGCTGCT ACGGGCCCTT CGGTCTCTCT 360
35 CCGCCAGCC AGGCGTCATC CGGCCAGGCC AGGATGTTT CTAACGCGCC CTACCTGCCC 420
AGCTGCCTCG AGAGCCAGCC CGCTATTCGC AATCAGG 457

SEQ ID NO: 11

Sequence length: 123

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence characteristic: Exon 2 of WT1 gene

Sequence:

GTTACAGCAC GGTCACCTTC GACGGGACGC CCAGCTACGG TCACACGCCC TCGCACCATG 60
CGGCGCAGTT CCCAACCAC TCATTCAAGC ATGAGGATCC CATGGGCCAG CAGGGCTCGC 120
50 TGG 123

SEQ ID NO: 12

Sequence length: 103

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence characteristic: Exon 3 of WT1 gene

Sequence:

GTGAGCAGCA GTACTCGGTG CCGCCCCCGG TCTATGGCTG CCACACCCCC ACCGACAGCT 60

GCACCGGCAG CCAGGCTTTG CTGCTGAGGA CGCCCTACAG CAG 103

SEQ ID NO: 13

Sequence length: 78

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence characteristic: Exon 4 of WT1 gene

Sequence:

TGACAATTTA TACCAAATGA CATCCCAGCT TGAATGCATG ACCTGGAATC AGATGAACTT 60

AGGAGCCACC TTAAAGGG 78

SEQ ID NO: 14

Sequence length: 51

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence characteristic: Exon 5 of WT1 gene

Sequence:

AGTTGCTGCT GGGAGCTCCA GCTCAGTGAA ATGGACAGAA GGGCAGAGCA A 51

SEQ ID NO: 15

Sequence length: 97

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence characteristic: Exon 6 of WT1 gene

Sequence:

CCACAGCACA GGGTACGAGA GCGATAACCA CACAACGCCC ATCCTCTGCG GAGCCCAATA 60

CAGAATACAC ACGCACGGTG TCTTCAGAGG CATTGAG 97

SEQ ID NO: 16

Sequence length: 151

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence characteristic: Exon 7 of WT1 gene

Sequence:

GATGTGCGAC GTGTGCCTGG AGTAGCCCCG ACTCTTGAC GGTCCGCATC TGAGACCAGT 60

GAGAAACGCC CCTTCATGTG TGCTTACCCA GGCTGCAATA AGAGATATTT TAAGCTGTCC 120

CACTTACAGA TGCACAGCAG GAAGCACACT G 151

SEQ ID NO: 17

Sequence length: 90

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence characteristic: Exon 8 of WT1 gene

Sequence:

GTGAGAAACC ATACCAGTGT GACTTCAAGG ACTGTGAACG AAGGTTTTCT CGTTCAGACC 60

AGCTCAAAAG ACACCAAAGG AGACATACAG 90

SEQ ID NO: 18

Sequence length: 93

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence characteristic: Exon 9 of WT1 gene

Sequence:

GTGTGAAACC ATTCCAGTGT AAAACTTGTC AGCGAAAGTT CTCCCGGTCC GACCACCTGA 60

AGACCCACAC CAGGACTCAT ACAGGTAAAA CAA 93

SEQ ID NO: 19

Sequence length: 158

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence characteristic: Portion of Exon 10 of WT1 gene

Sequence:

GTGAAAAGCC CTTAGCTGT CGGTGGCCAA GTTGTGAGAA AAAGTTTGCC CGGTCAGATG 60

AATTAGTCCG CCATCACAAC ATGCATCAGA GAAACATGAC CAAACTCCAG CTGGCGCTTT 120

GAGGGGTCTC CCTCGGGGAC CGTTCAGTGT CCCAGGCA 158

SEQ ID NO: 20

Sequence length: 18

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence:

AGAGAAGAAG GGAACCCC

SEQ ID NO: 21

Sequence length: 18

Sequence type: Nucleic acid

Strandedness: Single strand

Molecular type: Synthetic DNA

Sequence:

GCGTGGGCAG CCTGGGAA

SEQ ID NO: 22

Sequence length: 16

Sequence type: Amino acid

Molecular type: Synthetic peptide

Sequence:

Lys His Glu Asp Pro Met Gly Gln Gln Gly Ser Leu Gly Glu Gln Gln

5

10

15

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: KISHIMOTO, TADAMITSU
- (B) STREET: 3-5-31, NAKANO-CHO
- (C) CITY: TONDABAYASHI-SHI
- (D) STATE: OSAKA
- (E) COUNTRY: JAPAN
- (F) POSTAL CODE (ZIP): 562/JP

10

- (ii) TITLE OF INVENTION: LEUKEMIC CELL GROWTH INHIBITOR CONTAINING
ANTISENSE OLIGONUCLEOTIDE DERIVATIVE AGAINST WILMS' TUMOR
GENE (WT1)

15

- (iii) NUMBER OF SEQUENCES: 22

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

20

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 96914430.2

25

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

40

CCCACCGCAT TCGACCCT

18

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

50

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

AGGGTCGAAT GCGGTGGG

18

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCGGCCCCTC TTATTTGA

18

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TCAAATAAGA GGGGCCGG

18

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CAGCAAATGG GCTCCGAC

18

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GTCGGAGCCC ATTTGCTG

18

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGCGATAACC ACACAACG

18

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CGTTGTGTGG TTATCGCT

18

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs

EP 0 841 068 A1

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

	TGGTATCCTC GACCAGGGCC ACAGGCAGTG CTCGGCGGAG TGGCTCCAGG AGTTACCCGC	60
15	TCCCTGCCGG GCTTCGTATC CAAACCCTCC CCTTCACCCC TCCTCCCCAA ACTGGGCGCC	120
	AGGATGCTCC GGCCGGAATA TACGCAGGCT TTGGGCGTTT GCCAAGGGTT TTCTTCCCTC	180
	CTAAACTAGC CGCTGTTTTT CCGGCTTAAC CGTAGAAGAA TTAGATATTC CTCACTGGAA	240
20	AGGGAAACTA AGTGCTGCTG ACTCCAATTT TAGGTAGGCG GCAACCGCCT TCCGCCTGGC	300
	GCAAACCTCA CCAAGTAAAC AACTACTAGC CGATCGAAAT ACGCCCGGCT TATAACTGGT	360
	GCAACTCCCG GCCACCCAAC TGAGGGACGT TCGCTTTCAG TCCCGACCTC TGGAACCCAC	420
25	AAAGGGCCAC CTCTTTCCCC AGTGACCCCA AGATCATGGC CACTCCCCCTA CCCGACAGTT	480
	CTAGAGCAAG AGCCAGACTC AAGGGTGCAA AGCAAGGGTA TACGCTTCTT TGAAGCTTGA	540
30	CTGAGTTCTT TCTGCGCTTT CCTGAAGTTC CCGCCCTCTT GGAGCCTACC TGCCCCTCCC	600
	TCCAAACCAC TCTTTTAGAT TAACAACCCC ATCTCTACTC CCACCGCATT CGACCCTGCC	660
	CGGACTCACT GCTACTGAAC GGACTCTCCA GTGAGACGAG GCTCCCACAC TGGCGAAGGC	720
35	AAGAAGGGGA GGTGGGGGGA GGGTTGTGCC ACACCGGCCA GCTGAGAGCG CGTGTGGGT	780
	TGAAGAGGAG GGTGTCTCCG AGAGGGACGC TCCCTCGGAC CCGCCCTCAC CCCAGCTGCG	840
	AGGGCGCCCC CAAGGAGCAG CGCGCGCTGC CTGGCCGGGC TTGGGCTGCT GAGTGAATGG	900
40	AGCGGCCGAG CCTCCTGGCT CCTCCTCTTC CCCGCGCCGC CGGCCCCCTCT TATTTGAGCT	960
	TTGGGAAGCT GAGGGCAGCC AGGCAGCTGG GGTAAGGAGT TCAAGGCAGC GCCCACACCC	1020
	GGGGGCTCTC CGCAACCCGA CCGCCTGTGC CTCCCCACT TCCCGCCCTC CCTCCACCT	1080
45	ACTCATTCAC CCACCCACCC ACCCAGAGCC GGGACGGCAG CCCAGGCGCC CGGGCCCCGC	1140
	CGTCTCCTCG CCGCGATCCT GGACTTCCTC TTGCTGCAGG ACCCGGCTTC CACGTGTGTC	1200
	CCGGAGCCGG CGTCTCAGCA CACGCTCCGC TCCGGGCCTG GGTGCCTACA GCAGCCAGAG	1260
50	CAGCAGGGAG TC	1272

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

TCTGAGCCTC AGCAAATGGG CTCCGACGTG CGGGACCTGA ACGCGCTGCT GCCCGCCGTC      60
CCCTCCCTGG GTGGCGGCGG CGGCTGTGCC CTGCCTGTGA GCGGCGCGGC GCAGTGGGCG      120
CCGGTGCTGG ACTTTGCGCC CCCGGGCGCT TCGGCTTACG GGTTCGTTGGG CGGCCCCGCG      180
CCGCCACCGG CTCCGCCGCC ACCCCCGCCG CCGCCGCCTC ACTCCTTCAT CAAACAGGAG      240
CCGAGCTGGG GCGGCGCGGA GCCGCACGAG GAGCAGTGCC TGAGCGCCTT CACTGTCCAC      300
TTTTCCGGCC AGTTCACTGG CACAGCCGGA GCCTGTCGCT ACGGGCCCTT CGGTCCTCCT      360
CCGCCCAGCC AGGCGTCATC CGGCCAGGCC AGGATGTTTC CTAACGCGCC CTACCTGCCC      420
AGCTGCCTCG AGAGCCAGCC CGCTATTCGC AATCAGG                                457

```

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

GTTACAGCAC GGTCACCTTC GACGGGACGC CCAGCTACGG TCACACGCCC TCGCACCATG      60
CGGCGCAGTT CCCCAACCAC TCATTCAAGC ATGAGGATCC CATGGGCCAG CAGGGCTCGC      120
TGG                                123

```

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GTGAGCAGCA GTACTCGGTG CCGCCCCCGG TCTATGGCTG CCACACCCCC ACCGACAGCT 60
GCACCGGCAG CCAGGCTTTG CTGCTGAGGA CGCCCTACAG CAG 103

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TGACAATTTA TACCAAATGA CATCCCAGCT TGAATGCATG ACCTGGAATC AGATGAAGTT 60
AGGAGCCACC TTAAAGGG 78

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AGTTGCTGCT GGGAGCTCCA GCTCAGTGAA ATGGACAGAA GGGCAGAGCA A 51

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CCACAGCACA GGGTACGAGA GCGATAACCA CACAACGCCC ATCCTCTGCG GAGCCCAATA 60
CAGAATACAC ACGCACGGTG TCTTCAGAGG CATTGAG 97

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GATGTGCGAC GTGTGCCTGG AGTAGCCCCG ACTCTTGTAC GGTCGGCATC TGAGACCAGT 60
GAGAAACGCC CCTTCATGTG TGCTTACCCA GGCTGCAATA AGAGATATTT TAAGCTGTCC 120
CACTTACAGA TGCACAGCAG GAAGCACACT G 151

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GTGAGAAACC ATACCAAGTGT GACTTCAAGG ACTGTGAACG AAGGTTTTCT CGTTCAGACC 60
AGCTCAAAAG ACACCAAAGG AGACATACAG 90

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GTGTGAAACC ATTCCAGTGT AAAACTTGTC AGCGAAAGTT CTCCCGGTCC GACCACCTGA 60

AGACCCACAC CAGGACTCAT ACAGGTAAAA CAA 93

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GTGAAAAGCC CTTAGCTGT CGGTGGCCAA GTTGTCAGAA AAAGTTTGCC CGGTCAGATG 60

AATTAGTCCG CCATCACAAAC ATGCATCAGA GAAACATGAC CAAACTCCAG CTGGCGCTTT 120

GAGGGGTCTC CCTCGGGGAC CGTTCAGTGT CCCAGGCA 158

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AGAGAAGAAG GGAACCCC 18

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGTGGGCAG CCTGGGAA

18

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Lys	His	Glu	Asp	Pro	Met	Gly	Gln	Gln	Gly	Ser	Leu	Gly	Glu	Gln	Gln
1				5				10					15		

Claims

1. A growth inhibitor for leukemia cells containing an antisense nucleotide derivative to the Wilms' tumor gene (WT1).
2. A growth inhibitor for leukemia cells as set forth in claim 1 wherein said antisense oligonucleotide derivative is an antisense oligonucleotide to at least nine continuing nucleotides at the transcription capping site of the Wilms' tumor gene.
3. A growth inhibitor for leukemia cells as set forth in claim 2 wherein said antisense oligonucleotide derivative has the following nucleotide sequence:
 5'-AGGGTCTGAATGCGGTGGG-3' (SEQ ID NO: 2) or
 5'-TCAAATAAGAGGGGCCGG-3' (SEQ ID NO: 4).
4. A growth inhibitor for leukemia cells as set forth in claim 1 wherein said antisense oligonucleotide derivative is an antisense oligonucleotide to at least nine continuing nucleotides including the translation starting region of the Wilms' tumor gene.

5. A growth inhibitor of leukemia cells as set forth in claim 4 wherein said antisense oligonucleotide has the following nucleotide sequence:

5'-GTCGGAGCCCATTGCTG-3' (SEQ ID NO: 6).

- 5 6. A growth inhibitor for leukemia cells as set forth in claim 1 wherein said antisense oligonucleotide derivative is an antisense oligonucleotide corresponding to at least nine continuing nucleotides in an exon of the Wilms' tumor gene.

- 10 7. A growth inhibitor of leukemia cells as set forth in claim 6 wherein said exon is the 6th exon.

8. A growth inhibitor of leukemia cells as set forth in claim 7 wherein said antisense oligonucleotide derivative has the following nucleotide sequence:

5'-CGTTGTGTGTTATCGCT-3' (SEQ ID NO: 8).

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Fig.1

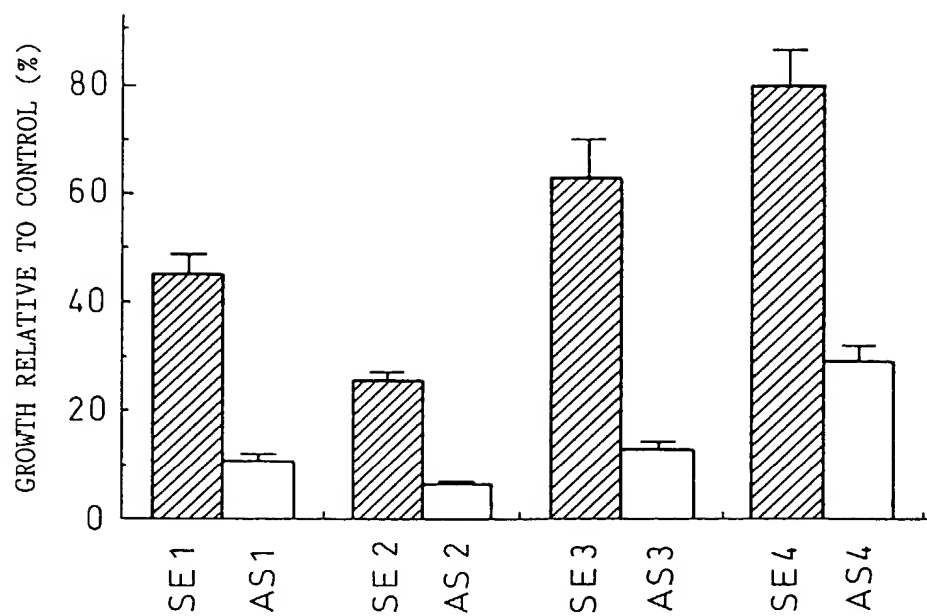


Fig.2

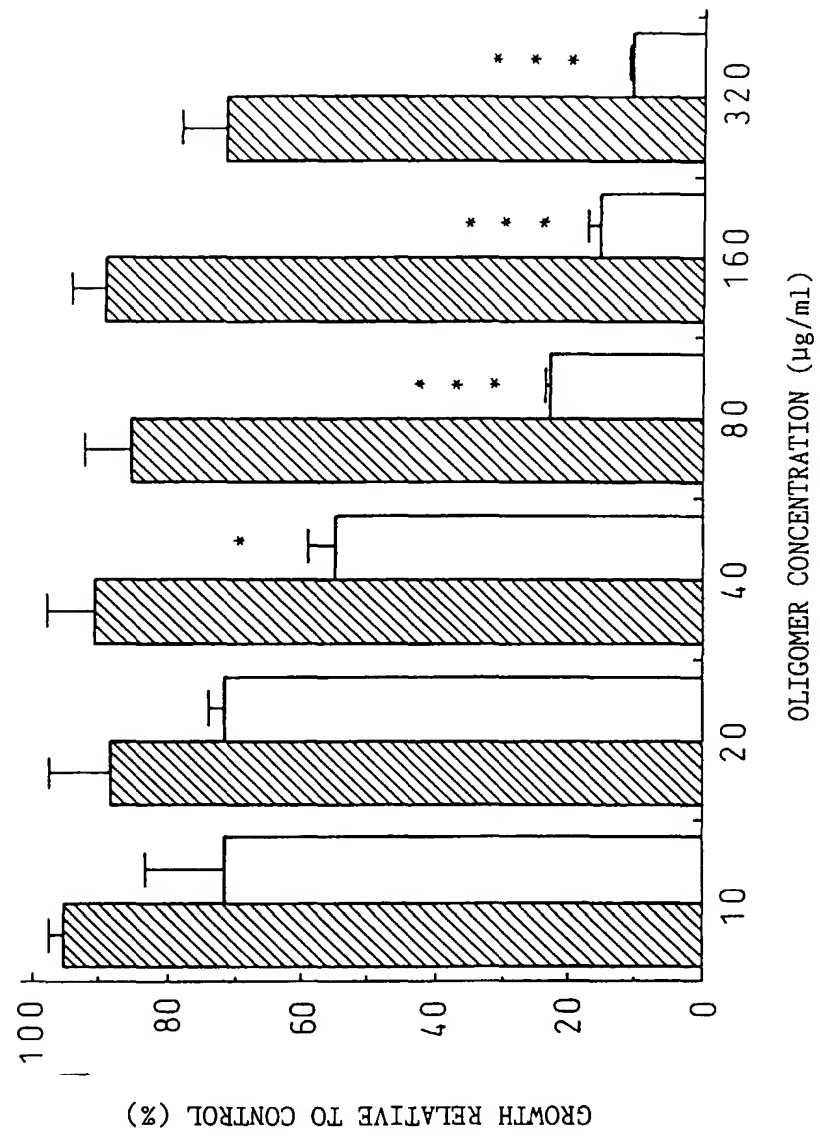


Fig.3

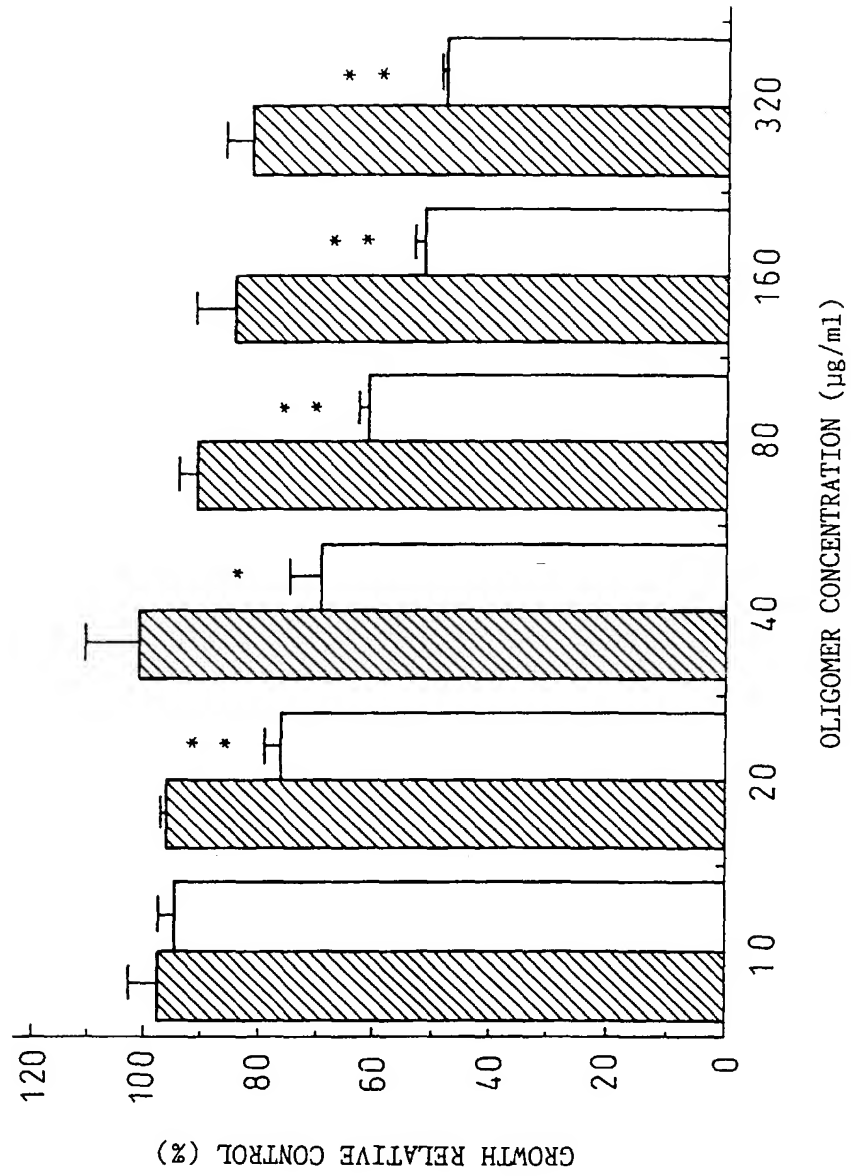


Fig.4

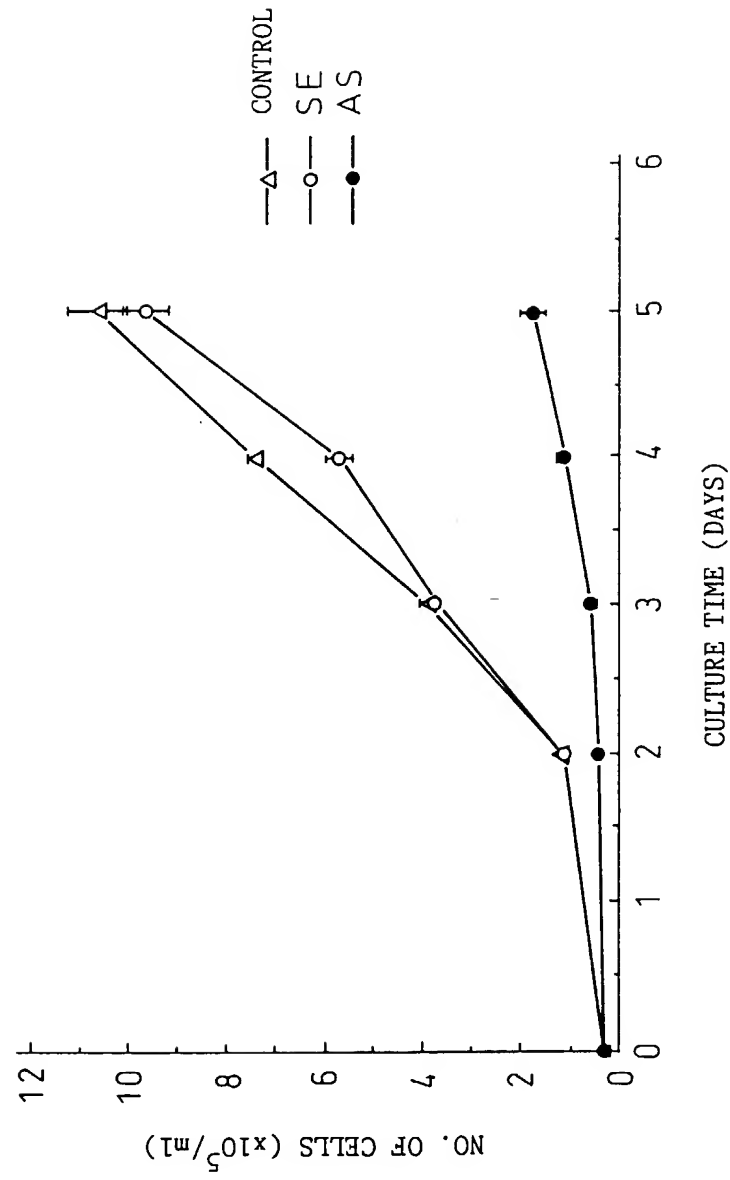


Fig.5

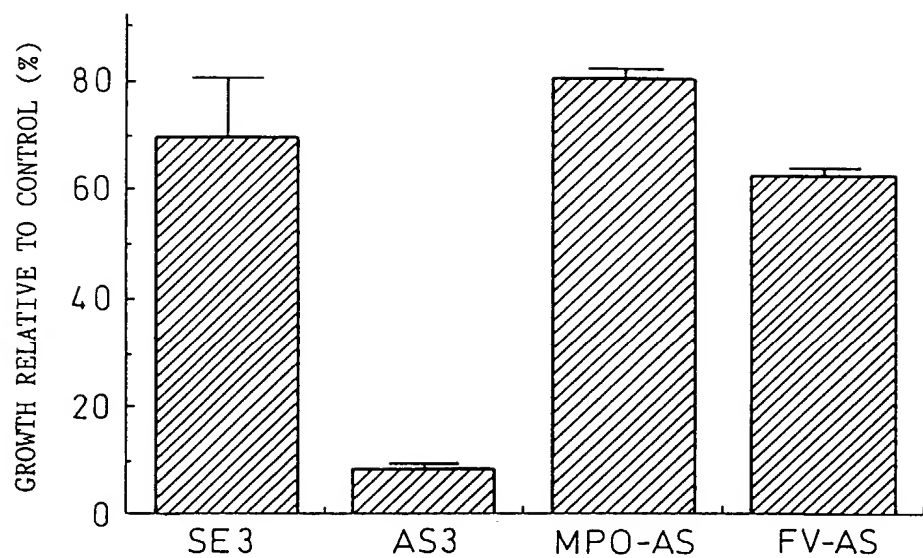


Fig.6

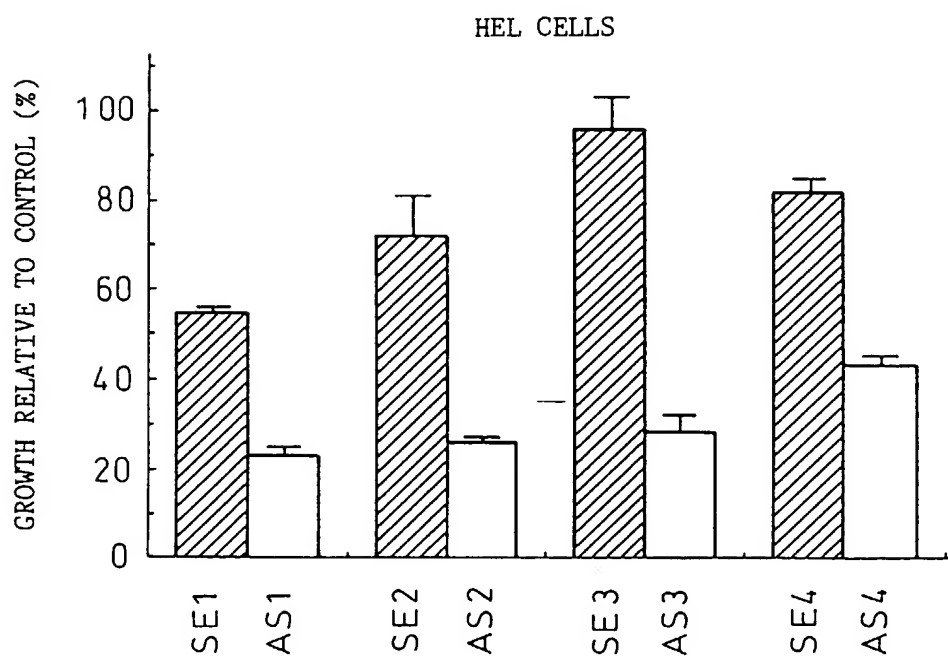


Fig.7

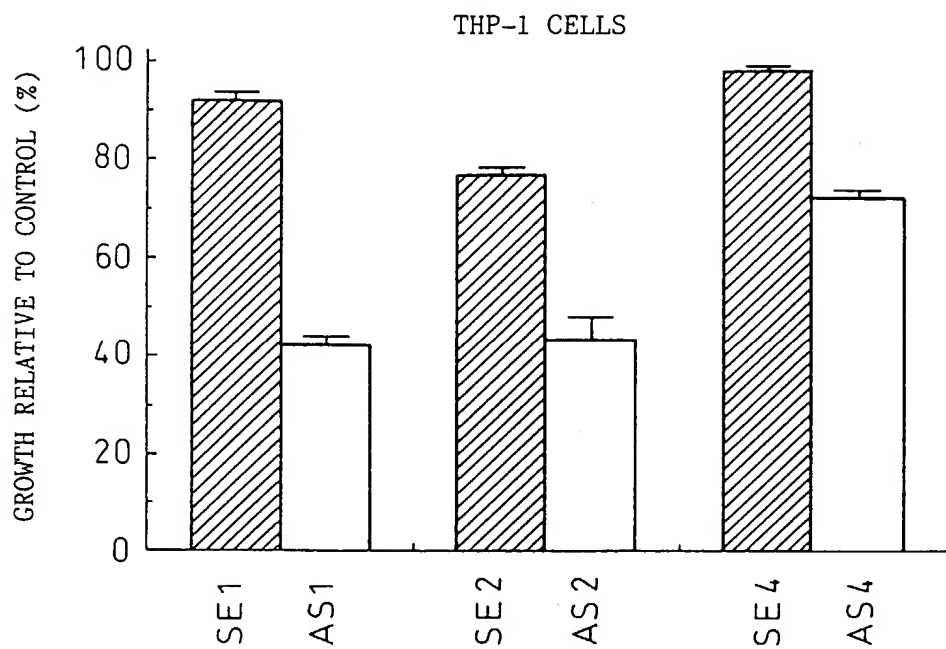


Fig.8

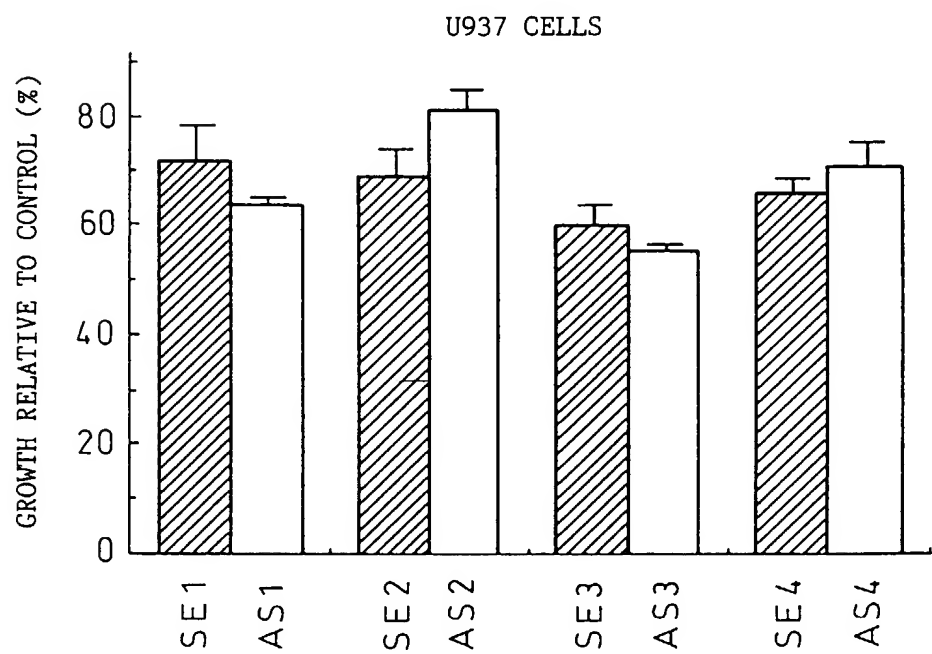


Fig.9

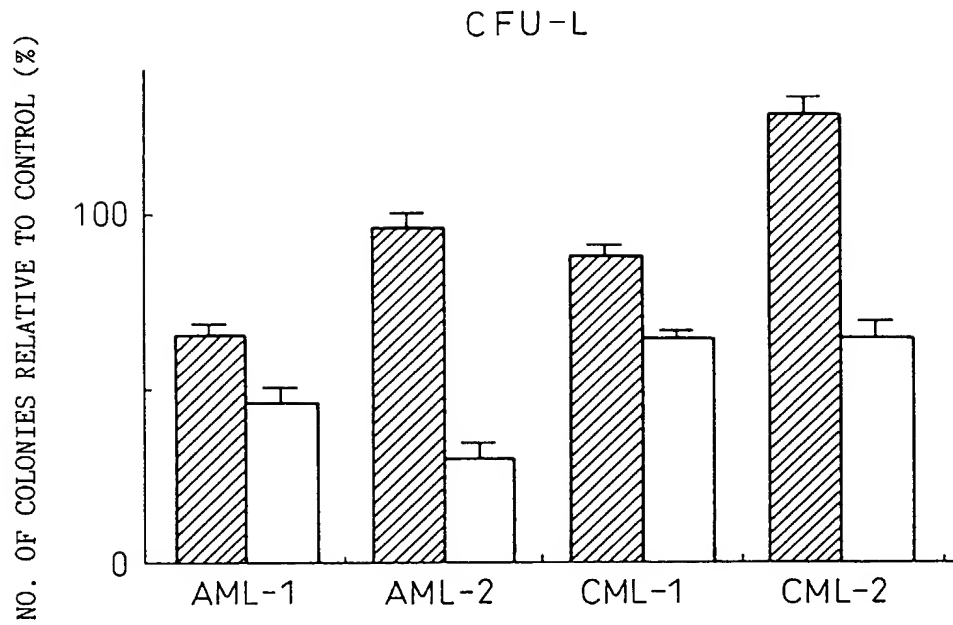


Fig.10

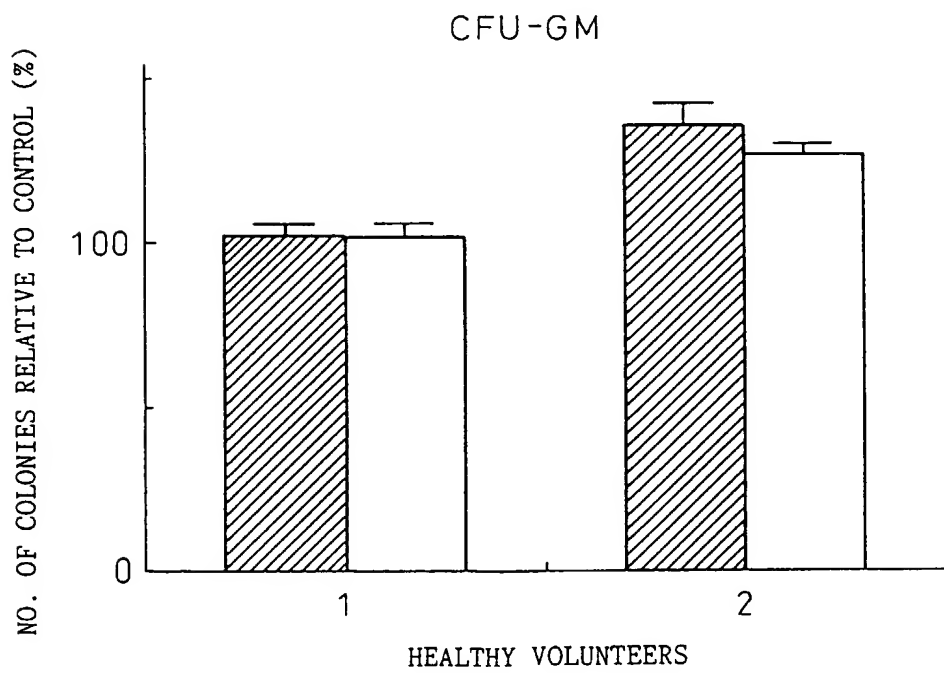
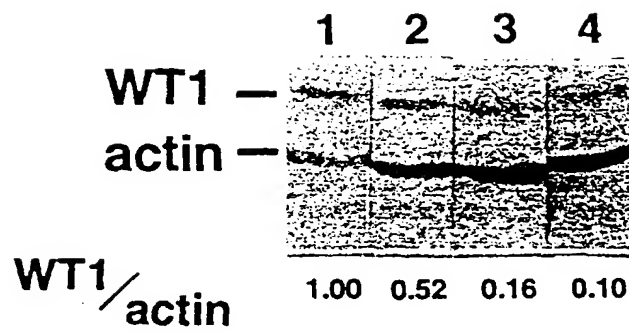
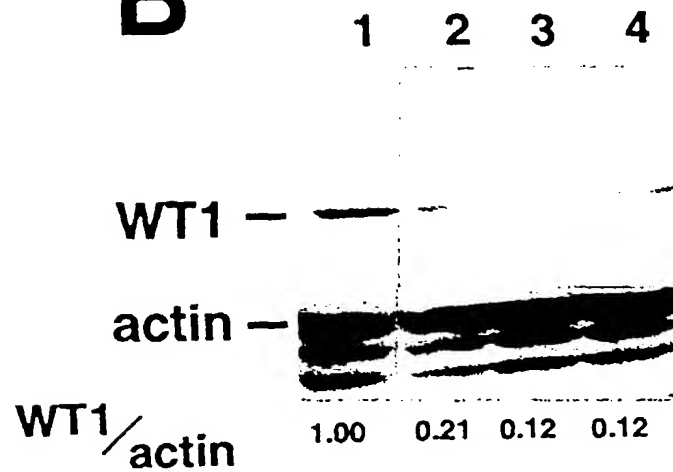


Fig. 11

A**B**

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP96/01394

A. CLASSIFICATION OF SUBJECT MATTER Int. Cl ⁶ A61K48/00, 31/70 // C07H21/02, 21/04, C12N15/11, 15/63 According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) Int. Cl ⁶ A61K48/00, 31/70 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) CAS ONLINE		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Blood, Vol. 84, No. 8 (1994), p. 2672-2680, (K. Inoue et al.)	1 - 8
Y	Blood, Vol. 84, No. 9 (1994), p. 3071-3079, (K. Inoue et al.)	1 - 8
Y	Human Molecular Genetics, Vol. 3, No. 9 (1994), p. 1633-1637, (K. Pritchard-Jones et al.),	1 - 8
Y	Nature, Vol. 343 (1990), p. 774-778, (M. Gessler et al.)	1 - 8
Y	Cell, Vol. 60, No. 3 (1990), p. 509-520, (K. M. Call et al.)	1 - 8
Y	Proc. Natl. Acad. Sci. USA., Vol. 88, No. 21 (1991), p. 9618-9622, (D. A. Haber et al.)	1 - 8
A	WO, 95/29995, A (Wistar Institute of Anatomy and Biology), November 9, 1995 (09. 11. 95) (Family: none)	1 - 8
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search August 13, 1996 (13. 08. 96)		Date of mailing of the international search report August 20, 1996 (20. 08. 96)
Name and mailing address of the ISA/ Japanese Patent Office Facsimile No.		Authorized officer Telephone No.

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP96/01394

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P	The Japanese Journal of Clinical Hematology, Vol. 36, No. 6 (1995), p. 552-228, (Kazushi Inoue, et al.)	1 - 8

Form PCT/ISA/210 (continuation of second sheet) (July 1992)